

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 27, 2004, 16:47:44 ; Search time 52 Seconds
(without alignments)
413.872 Million cell updates/sec

Title: US-10-063-688-34

Sequence: 1 MRYVLVIMKASVIMFVVL.....QVPRIONICTERNOPRN 678

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1017041 seqs, 315518202 residues

Word size: 6

Total number of hits satisfying chosen parameters: 8650

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database:

SPTREMBL_25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp Vertebrate:*
- 14: sp Unclassified:*
- 15: sp_rv1rus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	678	100.0	678	4 Q9UDNO	Q9UDNO homo sapien
2	411	60.6	693	4 Q96DM8	Q96DM8 mus musculu
3	259	38.2	656	4 Q96DT1	Q96DT1 mus musculu
4	57	8.4	652	6 Q95L12	Q95L12 bos taurus
5	45	6.6	628	11 Q9BQ41	Q9BQ41 mus musculu
6	45	6.6	650	11 Q9K047	Q9K047 mus musculu
7	45	6.6	650	11 Q9CY21	Q9CY21 mus musculu
8	45	6.6	650	11 Q9VH15	Q9VH15 mus musculu
9	11	1.6	553	13 Q9AM56	Q9AM56 brachydanio
10	8	1.2	100	10 Q9H8Y2	Q9H8Y2 oviza sativ
11	8	1.2	112	15 Q9G578	Q9G578 bifidobacte
12	8	1.2	174	16 Q9CB89	Q9CB89 mycobacteri
13	8	1.2	208	13 Q9QZ19	Q9QZ19 brachydanio
14	8	1.2	230	2 O54667	O54667 streptococc
15	8	1.2	230	2 Q8XWQ1	Q8XWQ1 streptococc
16	8	1.2	231	2 O86887	O86887 streptococc

17	8	1.2	231	2 Q9R1P2	Q9R1P2 streptococc
18	8	1.2	231	2 Q9AHD3	Q9AHD3 streptococc
19	8	1.2	285	16 Q92M09	Q92M09 rhizobium m
20	8	1.2	359	1 Q47973	Q47973 halobacteri
21	8	1.2	368	17 Q9HEU7	Q9HEU7 halobacteri
22	8	1.2	382	12 Q83907	Q83907 ovine adeno
23	8	1.2	391	16 Q98HP8	Q98HP8 rhizobium l
24	8	1.2	394	16 Q97FE4	Q97FE4 clostridium
25	8	1.2	400	16 Q7UD27	Q7UD27 shigella fl
26	8	1.2	416	5 Q8IRF0	Q8IRF0 drosophila
27	8	1.2	416	16 Q8FJ98	Q8FJ98 escherichia
28	8	1.2	416	16 Q83JN3	Q83JN3 shigella fl
29	8	1.2	461	3 Q9HRC6	Q9HRC6 neurospora
30	8	1.2	462	2 Q8RMG7	Q8RMG7 acetobacter
31	8	1.2	494	4 Q96T06	Q96T06 homo sapien
32	8	1.2	516	4 Q9H647	Q9H647 homo sapien
33	8	1.2	559	16 Q82114	Q82114 streptomyc
34	8	1.2	573	5 Q9GV07	Q9GV07 dugesia dor
35	8	1.2	686	5 Q9W013	Q9W013 drosophila
36	8	1.2	695	16 Q9CH87	Q9CH87 lactococcus
37	8	1.2	718	6 Q8XKH0	Q8XKH0 macaca fasc
38	8	1.2	763	5 Q960Y7	Q960Y7 drosophila
39	8	1.2	892	16 Q99PX4	Q99PX4 streptomyc
40	8	1.2	1078	5 Q9NDY3	Q9NDY3 leishmania
41	8	1.2	1464	5 Q9VX75	Q9VX75 drosophila
42	8	1.2	1464	5 Q96782	Q96782 drosophila
43	8	1.2	2197	5 Q9W016	Q9W016 drosophila
44	7	1.0	29	11 Q8VIF4	Q8VIF4 mus musculu
45	7	1.0	34	4 Q9H3R8	Q9H3R8 homo sapien

ALIGNMENTS

RESULT 1

ID	Q9UDNO	PRELIMINARY;	PRT;	678 AA.
AC	Q9UDNO			
DT	01-MAY-2000 (TREMBLrel. 13, Created)			
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)			
DE	Similar to Coch-SB2.			
GN	WDSC:H.NH029411.1.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RM	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=99063792; PubMed=9847074;			
RA	Sulston J.E., Waterston R.;			
RT	"Toward a complete human genome sequence.";			
RL	Genome Res. 8:1097-1108(1998).			
RM	[2]			
RP	SEQUENCE FROM N.A.			
RT	Cordes N., Kalicki J., Ames M.;			
RA	"The sequence of Homo sapiens BAC clone RP11-294111.";			
RL	Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.			
RM	[3]			
RP	SEQUENCE FROM N.A.			
RA	Waterston R.;			
RL	Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.			
RM	EMBL; AC007363; AAF19243.1; -.			
DR	HSSP; P11215; IJLM.			
DR	InterPro; IPR004043; LCCL dom.			
DR	InterPro; IPR002035; VWF_A.			
DR	Pfam; PF00092; VWA_2.			
DR	PRINTS; PR00453; VWFADOMAIN.			
DR	SMART; SM00603; LCCL; 1.			
DR	SMART; SM00327; VWA; 2.			
DR	PROSITE; PS50820; LCCL; 1.			
DR	PROSITE; PS50234; VWA; 2.			